Wilder 09/869,891

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=> d his 1

     (FILE 'MEDLINE, HCAPLUS, BIOSIS, EMBASE, WPIDS, SCISEARCH, AGRICOLA'
     ENTERED AT 15:08:46 ON 24 MAR 2004)
L21          89 DUP REM L20 (35 DUPLICATES REMOVED)

=> d que l21
L1           93 SEA PAQUIN B?/AU
L2         2373 SEA OLIGONUCLEOTID?(3A) LIBRAR?
L3            7 SEA L1 AND L2
L4         4203 SEA (POLYNUCLEOTID? OR OLIGONUCLEOTID?)(5A) LIBRAR?
L5          412 SEA L4 AND RANDOM?
L6           26 SEA L5 AND FLANK?
L8          131 SEA L5 AND (AMPLIF? OR PRIMER#)
L9            6 SEA L8 AND FIXED
L10          26 SEA L8 AND VARIA?
L18         130 SEA L3 OR L6 OR (L9 OR L10 OR L11 OR L12 OR L13 OR L14 OR L15)
                OR L17
L19           6 SEA L18 AND VARIABLE(5A) CHAIN#
L20         124 SEA L18 NOT L19
L21          89 DUP REM L20 (35 DUPLICATES REMOVED)


=> d ibib abs l21 1-89

L21  ANSWER 1 OF 89  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2004:60715  HCAPLUS
DOCUMENT NUMBER:          140:88698
TITLE:                    Methods for detection of nucleic acids using
                          PCR and probes immobilized to solid matrix
INVENTOR(S):              Scott, David L., Jr.
PATENT ASSIGNEE(S):       D-Squared Biotechnologies, Inc., USA
SOURCE:                   PCT Int. Appl., 18 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ----------------  ----  --------       ---------------  --------
     WO 2004007771      A1   20040122       WO 2002-US21660  20020710
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
             UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
             TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
             PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
             NE, SN, TD, TG
PRIORITY APPLN. INFO.:                    US 2002-304156P  P  20020710
AB   Methods for detection of nucleic acids using PCR and probes
     immobilized to solid matrix ar eprovided.  The unhybridized probe nucleic
     acid sequence is separated from the probe-target nucleic acid complex and the
     concentration of the unhybridized probe is determined  The use of nucleic acid
     pre-absorption assay with a random oligonucleotide
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Search completed by David Schreiber 308-4292

library is useful in identifying unique sequences in target nucleic acids.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 2 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2004-121562 [12] WPIDS
CROSS REFERENCE: 2003-901581 [82]
DOC. NO. CPI: C2004-048692
TITLE: Enriching low abundance polynucleotide relative to a high abundance polynucleotide in a sample, for analyzing gene expression and creating cDNA libraries, comprises blocking polymerase activity on high abundance polynucleotides.
DERWENT CLASS: B04 D16
INVENTOR(S): CHEN, C; SCHROEDER, B G; SCHROTH, G P
PATENT ASSIGNEE(S): (CHEN-I) CHEN C; (SCHR-I) SCHROEDER B G; (SCHR-I) SCHROTH G P
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2004014105	A1	20040122	(200412)*		62

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2004014105	A1 CIP of	US 2002-144179	20020509
		US 2003-435489	20030509

PRIORITY APPLN. INFO: US 2003-435489 20030509; US 2002-144179 20020509
AN 2004-121562 [12] WPIDS
CR 2003-901581 [82]
AB US2004014105 A UPAB: 20040218
NOVELTY - Enriching low abundance polynucleotide relative to a high abundance polynucleotide in a sample, where the ratio of the high abundance polynucleotide to the low abundance polynucleotide is at least 10:1, comprising blocking polymerase activity on high abundance polynucleotides by using enzymatically non-extendable nucleobase oligomers, is new.

DETAILED DESCRIPTION - Enriching low abundance polynucleotide relative to a high abundance polynucleotide in a sample, where the ratio of the high abundance polynucleotide to the low abundance polynucleotide is at least 10:1, comprising:

(a) exposing the sample to at least one first enzymatically non-extendable nucleobase oligomer having a nucleobase sequence complementary to a sequence within the high abundance polynucleotide under conditions such that base pairing occurs;

(b) exposing the sample to a primer having a nucleobase sequence complementary to a sequence within the low abundance polynucleotide under conditions such that base pairing occurs; and

(c) subjecting the sample to conditions for polymerase extension, so that the low abundance polynucleotide is amplified by extension of the primer and the high abundance polynucleotide is not amplified.

INDEPENDENT CLAIMS are also included for the following: